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## RAW SEQUENCE LISTING

DATE: 04/13/2001

PATENT APPLICATION: US/09/331,723A

TIME: 13:27:39

Input Set : A:\PTO.txt

Output Set: N:\CRF3\04122001\I331723A.raw

ENTERED

3 <110> APPLICANT: BOYNTON, John  
 4 GILLHAM, Nicholas  
 5 RANDOLPH-ANDERSON, Barbara  
 6 ISHIGE, Fumiharu  
 7 SATO, Ryo  
 9 <120> TITLE OF INVENTION: METHODS OF CONFERRING PPO-INHIBITING HERBICIDE RESISTANCE IN PLANTS BY  
 10 GENE MANIPULATION  
 12 <130> FILE REFERENCE: 2185-156P  
 14 <140> CURRENT APPLICATION NUMBER: US 09/331,723A  
 15 <141> CURRENT FILING DATE: 1999-08-18  
 17 <150> PRIOR APPLICATION NUMBER: PCT/US96/20415  
 18 <151> PRIOR FILING DATE: 1996-12-27  
 20 <160> NUMBER OF SEQ ID NOS: 24  
 22 <170> SOFTWARE: PatentIn version 3.0  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 47  
 26 <212> TYPE: PRT  
 27 <213> ORGANISM: Chlamydomonas reinhardtii  
 29 <220> FEATURE:  
 30 <221> NAME/KEY: misc\_feature  
 31 <223> OTHER INFORMATION: Strain CC-407  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: PEPTIDE  
 35 <222> LOCATION: (1)..(47)  
 36 <223> OTHER INFORMATION: product = porphyric herbicide resistance domain  
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 39 Ala Ala Glu Ala Leu Gly Ser Phe Asp Tyr Pro Pro Val Gly Ala Val  
 40 1 5 10 15  
 41 Thr Leu Ser Tyr Pro Leu Ser Ala Val Arg Glu Glu Arg Lys Ala Ser  
 42 20 25 30  
 43 Asp Gly Ser Val Pro Gly Phe Gly Gln Leu His Pro Arg Thr Gln  
 44 35 40 45  
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 47 <211> LENGTH: 46  
 48 <212> TYPE: PRT  
 49 <213> ORGANISM: Arabidopsis thaliana  
 51 <220> FEATURE:  
 52 <221> NAME/KEY: misc\_feature  
 53 <223> OTHER INFORMATION: ecotype Columbia  
 55 <220> FEATURE:  
 56 <221> NAME/KEY: PEPTIDE  
 57 <222> LOCATION: (1)..(46)  
 58 <223> OTHER INFORMATION: product = porphyric herbicide resistance domain  
 60 <400> SEQUENCE: 2  
 61 Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro Val Ala Ala Val  
 62 1 5 10 15  
 63 Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu Cys Leu Ile Asp

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65 Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln
66          35          40          45
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69 <211> LENGTH: 46
70 <212> TYPE: PRT
71 <213> ORGANISM: Zea mays
73 <220> FEATURE:
74 <221> NAME/KEY: misc_feature
75 <223> OTHER INFORMATION: Strain B73 inbred
77 <220> FEATURE:
78 <221> NAME/KEY: PEPTIDE
79 <222> LOCATION: (1)..(46)
80 <223> OTHER INFORMATION: product = porphyric herbicide resistance domain
82 <400> SEQUENCE: 3
83 Ala Ala Asp Ala Leu Ser Arg Phe Tyr Tyr Pro Pro Val Ala Ala Val
84 1          5          10          15
85 Thr Val Ser Tyr Pro Lys Glu Ala Ile Arg Lys Glu Cys Leu Ile Asp
86          20          25          30
87 Gly Glu Leu Gln Gly Phe Gly Gln Leu His Pro Arg Ser Gln
88          35          40          45
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91 <211> LENGTH: 141
92 <212> TYPE: DNA
93 <213> ORGANISM: Chlamydomonas reinhardtii
95 <220> FEATURE:
96 <221> NAME/KEY: misc_feature
97 <223> OTHER INFORMATION: Strain CC-407
99 <220> FEATURE:
100 <221> NAME/KEY: misc_feature
101 <222> LOCATION: (1)..(141)
102 <223> OTHER INFORMATION: encodes porphyric herbicide resistance domain
104 <400> SEQUENCE: 4
105 gccgccgagg ccctgggctc ottegactac ccgccggtgg gcgccgtgac gctgtcgtac 60
106 ccgctgagcg ccgtgcggga ggagcgcaag gcctcggacg ggtccgtgcc gggcttcggt 120
107 cagctgcacc cgcgcacgca g 141
110 <210> SEQ ID NO: 5
111 <211> LENGTH: 138
112 <212> TYPE: DNA
113 <213> ORGANISM: Arabidopsis thaliana
115 <220> FEATURE:
116 <221> NAME/KEY: misc_feature
117 <223> OTHER INFORMATION: ecotype Columbia
119 <220> FEATURE:
120 <221> NAME/KEY: misc_feature
121 <222> LOCATION: (1)..(138)
122 <223> OTHER INFORMATION: encodes porphyric herbicide resistance domain
124 <400> SEQUENCE: 5
125 gctgcaaagt cactctcaaa actatattac ccaccagttg cagcagtatc tatctcgtac 60

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126 ccgaaagaag caatccgaac agaattgttg atagatggtg aactaaaggg ttttgggcaa      120
127 ttgcatccac gcacgcaa                                     138
130 <210> SEQ ID NO: 6
131 <211> LENGTH: 138
132 <212> TYPE: DNA
133 <213> ORGANISM: Zea mays
135 <220> FEATURE:
136 <221> NAME/KEY: misc_feature
137 <223> OTHER INFORMATION: Strain B73 inbred
139 <220> FEATURE:
140 <221> NAME/KEY: misc_feature
141 <222> LOCATION: (1)..(138)
142 <223> OTHER INFORMATION: encodes porphyric herbicide resistance domain
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146 ccaaaggaag caattagaaa agaattgctta attgatgggg aactccaggg ctttggccag      120
147 ttgcatccac gtagtcaa                                     138
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152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <221> NAME/KEY: misc_feature
157 <222> LOCATION: (1)..(36)
158 <223> OTHER INFORMATION: Oligonucleotide primer for Arabidopsis thaliana
160 <400> SEQUENCE: 7
161 ctatattacc caccaatggc agcagtatct atctcg                                     36
164 <210> SEQ ID NO: 8
165 <211> LENGTH: 38
166 <212> TYPE: DNA
167 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
170 <221> NAME/KEY: misc_feature
171 <222> LOCATION: (1)..(38)
172 <223> OTHER INFORMATION: Oligonucleotide primer for Zea mays
174 <400> SEQUENCE: 8
175 gattctatta tccaccgatg gctgctgtaa ctgtttcg                                     38
178 <210> SEQ ID NO: 9
179 <211> LENGTH: 26
180 <212> TYPE: DNA
181 <213> ORGANISM: Artificial Sequence
183 <220> FEATURE:
184 <221> NAME/KEY: misc_feature
185 <222> LOCATION: (1)..(26)
186 <223> OTHER INFORMATION: Oligonucleotide primer common to both of A. thaliana and Z. mays
187     porphyric herbicide resistance domain of PP
189 <220> FEATURE:
190 <221> NAME/KEY: misc_feature
191 <222> LOCATION: (1)..(26)

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192 <223> OTHER INFORMATION: "n" residues can be inosine in addition to G, A, T or C; "k" at  
 193 position 1 is equal to G or T; "y" at positions 3 and 6 is equal  
 194 to C or T; "s" at positions 17 and 26 is equal to C or G; and "w"  
 195 at position 25 is equal to A or T

197 &lt;400&gt; SEQUENCE: 9

198 kaytayccnc cnatggsngc ngtnws

26

201 &lt;210&gt; SEQ ID NO: 10

202 &lt;211&gt; LENGTH: 2573

203 &lt;212&gt; TYPE: DNA

204 &lt;213&gt; ORGANISM: Chlamydomonas reinhardtii

206 &lt;220&gt; FEATURE:

207 &lt;221&gt; NAME/KEY: misc\_feature

208 &lt;223&gt; OTHER INFORMATION: Strain RS-3

210 &lt;220&gt; FEATURE:

211 &lt;221&gt; NAME/KEY: misc\_feature

212 &lt;222&gt; LOCATION: (1)..(2573)

213 &lt;223&gt; OTHER INFORMATION: encodes protoporphyrinogen oxidase

215 &lt;400&gt; SEQUENCE: 10

216	ctcgagagcg	ttggaggaaa	tccgtttggc	acctgttccg	gcttctttgt	gtgcacggcc	60
217	acgtccccct	ttcctgctac	ccgtccccc	ccggttttac	tgcccccttc	actcctcggc	120
218	tccatcccg	ttccatccgc	tcctcctccc	ccacctagac	tgtctaccgt	ctaccagttt	180
219	cttgggcaat	cattaacgta	accccgccctc	cctgcgcctg	ccctccctc	cctctccccc	240
220	ccgcacagcc	cgccgcccgc	gaggccctgg	gtccttcga	ctaccgcgcg	atggggcgccg	300
221	tgcagctgtc	gtaccgcgtg	agcgccgtgc	gggaggagcg	caaggcctcg	gacgggtccg	360
222	tgccgggctt	cggtcagctg	caccgcgcga	cgcaaggtag	caagtgcgcg	cgtgttgccg	420
223	cggtgtgttt	gcggagggga	gggtgtggg	ggttgggggt	gggggtggg	gggattggg	480
224	cgctgggtcg	tatcccgcg	ttgtatcctc	gcgctccct	catccattcc	ccccttcaac	540
225	aacacacacg	ggcgacacg	caccctcttt	gcgcttactt	tgtctggtgc	tccttaaac	600
226	actcttgcgt	tcatttttgt	gtcttctaac	acacacactt	gtccacacac	agggcatcac	660
227	cactctgggc	accatctaca	gtccagcct	gttccccggc	cgcgcgcgcg	agggccacat	720
228	gctgctgtc	aactacatcg	gcggcaccac	caaccgcggc	atcgtcaacc	agaccaccga	780
229	gcagctggtg	gagcaggtgt	gtgtgtggg	gggtggggg	ggggcagtg	atttttggg	840
230	tgagccccct	gagcaaacg	atccagggg	ggcgaagcc	cccaggattg	cccctgtccg	900
231	tgcgtgctgt	tgtgctgtg	tcgacaaaa	gtaccgtact	ggcacaaacc	gcgagtgcga	960
232	cgtattatta	attgcaatta	cctattgtag	aaaaatagac	ggcagggaaa	actcggccgg	1020
233	agcgagaagc	gacctcgtga	gtccatggac	atcttgactt	tcttcagttc	gcgagtata	1080
234	ctctcggccc	ctaaatatct	tacatccatg	tatcaaaa	tgctgcagac	aagcgtcttg	1140
235	gggcaagaat	gtcgaaattg	tttgcaacag	ccaaaccatg	cgtccccgag	ccttacatgt	1200
236	gtcgcggccc	gggatcccg	gcccagccc	ggctagccct	ttgcggtgct	tgagtgggat	1260
237	gtgggtgagg	tgcatttggg	atatcatgga	ccgtgaagtg	gcgtgggtaa	ggtggcgtgg	1320
238	cgtggcgggg	acagggcatg	tcggtgcctc	ggcacagcgt	tggectagtg	gccagtcccg	1380
239	ctggatgggc	ttgcaagggt	gctgttcatg	tcgccggtgc	ccatcgtcac	atccccttgc	1440
240	gtacatggg	gtcagcccca	ttttccagct	gtacaaagct	gacaccctt	gttgtgtggc	1500
241	gtcttggacc	cgtgttgett	cggagetggc	cagaaccccc	tgtgggcaca	cacacgcaca	1560
242	cacacacaca	cacacacaca	cacacacaca	cacacacaca	cacacacaca	cacacacaca	1620
243	cacacacaca	cacacacaca	cacacacaca	cacacacaca	cacattttcg	tcctgcagcc	1680
244	ccgaaccccc	cgcccggttc	cacgtcttcc	acctgcgcga	ccccccccc	tgccgcacgc	1740
245	ctgctctcac	cgctctccc	cccaccccat	ctccctgcag	gtggacaagg	acctgcgcaa	1800
246	catggtcatc	aagcccgcag	cgcccaagcc	ccgtgtggtg	ggcgtgcgcg	tgtggccgcg	1860

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247 cgccatcccg cagggtgtgag ggcgcagcag ccggagggat gggctagatc ctagttttctc 1920
248 aaagagctct acagccctat aacctcgacc tgcgaccttc gacctgataa cctggctgcc 1980
249 ccctcccaac ctagccacct ctccccggat ttgggttcac tcggttgact tgcttttggg 2040
250 ttctggaatc aacttcacct gttgtatact ttgctgcaact tctctgtacc actotttgca 2100
251 ttaggttcgg tttagtttg gctgcatgtg taacctctcc tccccgccct gccacctgca 2160
252 gttcaacctg ggccacctgg agcagctgga caaggcgcg c aaggcgctgg acgcggcggg 2220
253 gctgcagggc gtgcacctgg ggggcaacta cgtcagcggg gagcgcgctgg gcagcagcag 2280
254 cagcaggaag aggggagggg aggggagggg aggggtacaag gaggaggttg agcaggaggt 2340
255 ggtgctaagg cgcaaagcaa ggcggtgttg tatcctcatt gactgaaacc gggaaacca 2400
256 gcatgaacaa gaggtcaggg gactgcaagg agcggaggct acatgtatga ctacccccga 2460
257 cgcgggcgat gattccttga ctattgggac ctatttcgtt gggctcgggc acatgacccc 2520
258 cctggccccct tcgctgtatg gtgccagcc gccagccgc cccccgccca cac 2573
261 <210> SEQ ID NO: 11
262 <211> LENGTH: 1704
263 <212> TYPE: DNA
264 <213> ORGANISM: Arabidopsis thaliana
266 <220> FEATURE:
267 <221> NAME/KEY: misc_feature
268 <223> OTHER INFORMATION: ecotype Columbia
270 <220> FEATURE:
271 <221> NAME/KEY: CDS
272 <222> LOCATION: (16)..(1629)
273 <223> OTHER INFORMATION: product = protoporphyrinogen oxidase
275 <400> SEQUENCE: 11
276 ttctctgcga ttcc atg gag tta tct ctt ctc cgt ccg acg act caa tcg 51
277 Met Glu Leu Ser Leu Leu Arg Pro Thr Thr Gln Ser
278 1 5 10
279 ctt ctt ccg tcg ttt tcg aag ccc aat ctc cga tta aat gtt tat aag 99
280 Leu Leu Pro Ser Phe Ser Lys Pro Asn Leu Arg Leu Asn Val Tyr Lys
281 15 20 25
282 cct ctt aga ctc cgt tgt tca gtg gcc ggt gga cca acc gtc gga tct 147
283 Pro Leu Arg Leu Arg Cys Ser Val Ala Gly Gly Pro Thr Val Gly Ser
284 30 35 40
285 tca aaa atc gaa ggc gga gga ggc acc acc atc acg acg gat tgt gtg 195
286 Ser Lys Ile Glu Gly Gly Gly Gly Thr Thr Ile Thr Thr Asp Cys Val
287 45 50 55 60
288 att gtc ggc gga ggt att agt ggt ctt tgc atc gct cag gcg ctt gct 243
289 Ile Val Gly Gly Gly Ile Ser Gly Leu Cys Ile Ala Gln Ala Leu Ala
290 65 70 75
291 act aag cat cct gat gct gct ccg aat tta att gtg acc gag gct aag 291
292 Thr Lys His Pro Asp Ala Ala Pro Asn Leu Ile Val Thr Glu Ala Lys
293 80 85 90
294 gat cgt gtt gga ggc aac att atc act cgt gaa gag aat ggt ttt ctc 339
295 Asp Arg Val Gly Gly Asn Ile Ile Thr Arg Glu Glu Asn Gly Phe Leu
296 95 100 105
297 tgg gaa gaa ggt ccc aat agt ttt caa ccg tct gat cct atg ctc act 387
298 Trp Glu Glu Gly Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr
299 110 115 120
300 atg gtg gta gat agt ggt ttg aag gat gat ttg gtg ttg gga gat cct 435

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L:198 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9